Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	716	southern with blot same bacter$4 same detect$4	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L2	591	southern with blot same bacter$4 same detect$4 same pcr	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43
L3	26	southern with blot same bacter$4 same detect$4 same pcr same sample	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2005/05/05 10:43

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   [Align]

Sequence 1	lcl|seq_1		**Length** 20 (1 .. 20)
Sequence 2	gi 1799980	E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.).	**Length** 16446 (1 .. 16446)
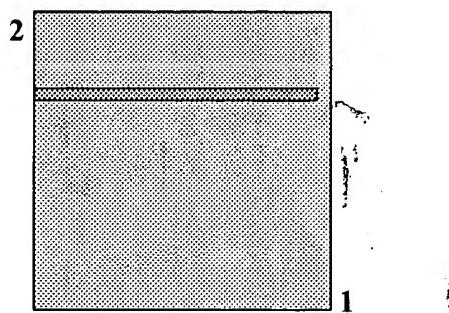
2

1

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 39.1 bits (20), Expect = 0.046
Identities = 20/20 (100%)
 Strand = Plus / Minus
```

```
Query: 1      ttcgggttgtcatgccaatg 20
              ||||||||||||||||||||
Sbjct: 11799  ttcgggttgtcatgccaatg 11780
```

SEQ ID NO 2

YAMAMOTO etal.

```
CPU time:      0.01 user secs.      0.00 sys. secs      0.01 total secs.

Lambda    K       H
   1.33    0.621    1.12

Gapped
Lambda    K       H
   1.33    0.621    1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 5
```

```
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 20
Length of database: 13,936,275,478
Length adjustment: 18
Effective length of query: 2
Effective length of database: 13,936,275,460
Effective search space: 27872550920
Effective search space used: 27872550920
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 16 (31.5 bits)
```

Blast 2 Sequences results

NCBI
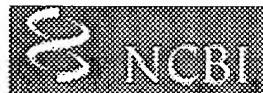
PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   [Align]

Sequence 1   lcl|seq_1   **Length** 18   (1 .. 18)

Sequence 2   gi 1799980   E.coli genomic DNA, Kohara clone #436(58.4-58.8 min.).   **Length** 16446   (1 .. 16446)
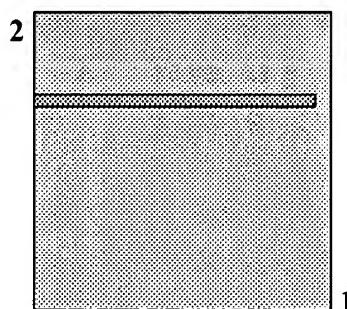
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 35.3 bits (18), Expect = 0.66
Identities = 18/18 (100%)
 Strand = Plus / Plus
```

```
Query: 1       ccgccaggcaaattctgt 18          SEQ ID NO 25
               ||||||||||||||||||
Sbjct: 11482   ccgccaggcaaattctgt 11499       YAMAMOTO et al.
```

```
CPU time:      0.01 user secs.      0.01 sys. secs      0.02 total secs.

Lambda      K        H
   1.33      0.621      1.12

Gapped
Lambda      K        H
   1.33      0.621      1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 4
```

```
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 18
Length of database: 13,936,275,478
Length adjustment: 16
Effective length of query: 2
Effective length of database: 13,936,275,462
Effective search space: 27872550924
Effective search space used: 27872550924
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 16 (31.5 bits)
```